

# **Genetic diversity among methicillin-resistant staphylococcus aureus in Malaysia (2002–2020)**

## **ABSTRACT**

Background: Methicillin-resistant Staphylococcus aureus (MRSA) is a common organism seen in both healthcare-associated and community-associated infections worldwide and in Malaysia over the past two decades. The aim of this review is to provide a firsthand documentation of all MRSA strains prevalent in the Malaysian population from 2002 to present and briefly describe the changing patterns. Methods: Electronic and manual intensive literature searches were conducted between 2002 and 2020, addressing issues directly related to patients and published in the English language were selected. Results: The literature search retrieved a total of 2217 articles and abstracts of 27 articles. The search yielded a total of 24 articles on genotyping of MRSA in Malaysia. The study found that MRSA strains were mostly genetically related and resulted in the predominant MRSA clones that caused active infections. Thirty-six different sequence types (ST) were recorded. The highest rates of STs detected were ST239 (52.6%), ST1 (47.4%), and ST22 (42.1%). The majority of studies showed that both SCCmec types III and IV were the most common SCCmec type in Malaysia, followed by SCCmec type V (57.9%). Conclusions: Both Brazilian (ST 239 IIIA) and Hungarian (ST 239-III) MRSA strains were detected in Malaysia. PFGE remains the best method for comparing MRSA strains. However, whole-genome sequencing has a promising chance to replace PFGE in the future.